

Abstract

A method for improving the reliability and/or accuracy of physical measurements obtained from array hybridization studies performed on
5 an array having a large number of genomic samples uses a small
number of replicates insufficient for making precise and valid
statistical inferences. This is overcome by estimating an error in
measurement of a sample by averaging errors obtained when measuring
the large number of samples or a subset of the large number of
10 samples. The estimated sample error is utilized as a standard for
accepting or rejecting the measurement of the respective sample.
The samples may be independent or dependant in that correlated
across two or more conditions.